

# Simple greedy 2-approximation algorithm for the maximum genus of a graph

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## Abstract

The maximum genus  $\gamma_M(G)$  of a graph  $G$  is the largest genus of an orientable surface into which  $G$  has a cellular embedding. Combinatorially, it coincides with the maximum number of disjoint pairs of adjacent edges of  $G$  whose removal results in a connected spanning subgraph of  $G$ . In this paper we prove that removing pairs of adjacent edges from  $G$  arbitrarily while retaining connectedness leads to at least  $\gamma_M(G)/2$  pairs of edges removed. This allows us to describe a greedy algorithm for the maximum genus of a graph; our algorithm returns an integer  $k$  such that  $\gamma_M(G)/2 \leq k \leq \gamma_M(G)$ , providing a simple method to efficiently approximate maximum genus. As a consequence of our approach we obtain a 2-approximate counterpart of Xuong's combinatorial characterisation of maximum genus.

**Keywords:** maximum genus, embedding, graph, greedy algorithm.

**AMS subject classification.** Primary: 05C10. Secondary: 05C85, 05C40.

## 1 Introduction

The *maximum genus*  $\gamma_M(G)$  of a graph  $G$  is the maximum integer  $g$  such that  $G$  has a cellular embedding in the orientable surface of genus  $g$ . A result of Duke [7] implies that a graph  $G$  has a cellular embedding in the orientable surface of genus  $g$  if and only if  $\gamma(G) \leq g \leq \gamma_M(G)$  where  $\gamma(G)$  denotes the (minimum) genus of  $G$ . The problem of determining the set of genera of orientable surfaces upon which  $G$  can be embedded thus reduces to calculation of  $\gamma(G)$  and  $\gamma_M(G)$ .

Computing the minimum genus of a graph is a notoriously difficult problem, which is known to be NP-complete even for cubic graphs (see [21, 22]). Nevertheless, the minimum genus can be calculated in linear time for graphs with bounded genus or bounded treewidth by [13]. Moreover, for graphs with fixed treewidth and bounded maximum degree [10] provides a polynomial-time algorithm obtaining the complete genus distribution  $\{g_i\}$  of the graph  $G$ , where  $g_i$  denotes the number of cellular embeddings of  $G$  into the orientable surface of genus  $i$ . For graphs of bounded maximum degree [2] has recently proposed a polynomial-time algorithm constructing an embedding with genus at most  $O(\gamma(G)^{c_1} \log^{c_2} n)$  where  $c_1$  and  $c_2$  are constants. On the other hand, for every  $\epsilon > 0$  and every function  $f(n) = O(n^{1-\epsilon})$  there is no polynomial-time algorithm that constructs an embedding of any graph  $G$  with  $n$  vertices into the surface of genus at most  $\gamma(G) + f(n)$  unless  $P = NP$  (see [4, 5]).

For maximum genus, the situation is quite different, as maximum genus admits a good (min-max) characterisation by Xuong's and Nebeský's theorems, see [15, 24] and [14, 17], respectively. From among these results the best known is Xuong's theorem stating that  $\gamma_M(G) = (\beta(G) - \min_T \text{odd}(G - E(T)))/2$ , where  $\beta(G)$  is the cycle rank of  $G$ ,  $\text{odd}(G - E(T))$  is the number of components of  $G - E(T)$  with an odd number of edges, and the minimum is taken over all spanning trees  $T$  of  $G$ . Building on these results, Furst et al. [8] and Glukhov [9] independently devised polynomial-time algorithms for determining the maximum genus of an arbitrary graph. The algorithm of [8] uses

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Xuong's characterisation of maximum genus and exploits a reduction to the linear matroid parity on an auxiliary graph; its running time is bounded by  $O(mn\Delta \log^6 m)$ , where  $n$ ,  $m$ , and  $\Delta$  are the number of vertices, edges, and the maximum degree of the graph, respectively. A matroidal structure is also in the background of the algorithm derived in [9], albeit in a different way. Starting with any spanning tree  $T$  of  $G$ , the algorithm greedily finds a sequence of graphs  $F_i$  such that  $T = F_0 \subseteq \dots \subseteq F_n \subseteq G$ ,  $|E(F_{i+1}) - E(F_i)| = 2$ , and  $\gamma_M(F_i) = i$  for all  $i$ , and  $\gamma_M(F_n) = \gamma_M(G)$ . The running time of this algorithm is bounded by  $O(m^6)$ .

Although two polynomial-time algorithms for the maximum genus problem are known, both are relatively complicated. It is therefore desirable to have a simpler way to determine the maximum genus, at least approximately. A greedy approximation algorithm for the maximum genus of a graph was proposed by Chen [3]. The algorithm has two main phases. First, it modifies a given graph  $G$  into a 3-regular graph  $H$  by vertex splitting, chooses an arbitrary spanning tree  $T$  of  $H$ , and finds a set  $P$  of disjoint pairs of adjacent edges in  $H - E(T)$  with the maximum possible size. Second, it constructs a single-face embedding of  $T \cup P$  and then inserts the remaining edges into the embedding while trying to raise the genus as much as possible. A high-genus embedding of  $G$  in the same surface is then constructed by contracting the edges created by vertex splitting. The algorithm constructs an embedding of  $G$  with genus at least  $\gamma_M(G)/4$  and its running time  $O(m \log n)$  is dominated by the second phase, that is, by operations on an embedded spanning subgraph of  $H$ .

In this paper we show that there is a much simpler way to approximate maximum genus. Our algorithm repeatedly removes arbitrary pairs of adjacent edges from  $G$  while keeping the graph connected. We prove that this simple idea leads to at least  $\gamma_M(G)/2$  pairs removed, providing an algorithm that returns an integer  $k$  such that  $\gamma_M(G)/2 \leq k \leq \gamma_M(G)$ . This process can be implemented with running time  $O(m^2 \log^2 n / (n \log \log n))$ . The algorithms developed in [3] can then be used to efficiently construct an embedding with genus  $k$ . Our result provides the first method to approximate maximum genus that can be easily implemented and improves the previous more complicated algorithm of Chen [3], which can guarantee embedding with genus only  $\gamma_M(G)/4$ . Structurally, our approach yields a natural 2-approximate counterpart of Xuong's theorem.

## 2 Background

In this section we present definitions and results that provide the background for our algorithm.

Our terminology is standard and consistent with [16]. By a graph we mean a finite undirected graph with loops and parallel edges permitted. Throughout, all embeddings into surfaces are cellular, forcing our graphs to be connected, and the surfaces are orientable. For more details and the necessary background we refer the reader to [11] or [16]; a recent survey of maximum genus can be found in [1, Chapter 2].

One of the earliest results on embeddings of graphs is the following observation, which is sometimes called Ringeisen's edge-addition lemma. Although it is implicit in [19], Ringeisen [20] was perhaps the first to draw an explicit attention to it.

**Lemma 1.** *Let  $\Pi$  be an embedding of a connected graph  $G$  and let  $e$  be an edge not contained in  $G$ , but incident with vertices in  $G$*

- (i) *If both ends of  $e$  are inserted into the same face of  $\Pi$ , then this face splits into two faces of the extended embedding of  $G + e$  and the genus does not change.*
- (ii) *If the ends of  $e$  are inserted into two distinct faces of  $\Pi$ , then in the extended embedding of  $G + e$  these faces are merged into one and the genus raises by one.*

The next lemma, independently obtained in [15], [12], and [24], constitutes the cornerstone of proofs of Xuong's theorem. It follows easily from Lemma 1.

**Lemma 2.** *Let  $G$  be a connected graph and  $\{e, f\}$  a pair of adjacent edges not contained in  $G$ , but incident with vertices in  $G$ . If  $G$  has an embedding with a single face, then so does  $G \cup \{e, f\}$ .*

Recall that by Xuong's theorem  $\gamma_M(G) = (\beta(G) - \min_T \text{odd}(G - E(T)))/2$ , where  $\text{odd}(G - E(T))$  is the number of components of the cotree  $G - E(T)$  with an odd number of edges. It is not difficult

to see that every cotree component with an even number of edges can be partitioned into pairs of adjacent edges, and that every cotree component with an odd number of edges can be partitioned into pairs of adjacent edges and one unpaired edge. Therefore, any spanning tree  $S$  minimising  $\text{odd}(G - E(T))$  maximises the number of pairs in the above partition of the cotree. The proof strategy of Xuong's theorem can now be summarised as follows. First, embed  $S$  in the 2-sphere arbitrarily. Then repeatedly apply Lemma 2 to pairs obtained from the partition of the components of  $G - E(S)$ , each time rising the genus by one. Finally, add the remaining edges. Lemma 1 guarantees that the addition cannot lower the genus. The result of this process is an embedding of  $G$  with genus at least  $(\beta(G) - \min_T \text{odd}(G - E(T)))/2$ .

The fact that a spanning tree minimising  $\text{odd}(G - E(T))$  maximises the number of pairs of adjacent edges in the cotree suggests a slightly different combinatorial characterisation of maximum genus. It is due to Khomenko et al. [15] and in fact is older than Xuong's theorem itself.

**Theorem 3.** *The maximum genus of a connected graph equals the maximum number of disjoint pairs of adjacent edges whose removal leaves a connected graph.*

The following useful lemma, found for example in [4], is an extension of Lemma 2 to embeddings with more than one face. It can either be proved directly by using Ringel's edge-adding technique or can be derived from Xuong's theorem. We may note in passing that this lemma was used in [4] to devise an algorithm that constructs an embedding of genus  $\gamma_M(G) - 1$  whenever such an embedding exists.

**Lemma 4.** *Let  $G$  be a connected graph and  $\{e, f\}$  a pair of adjacent edges not contained in  $G$ , but incident with vertices in  $G$ . Then  $\gamma_M(G \cup \{e, f\}) \geq \gamma_M(G) + 1$ .*

Our main observation is that Lemma 4 can be applied to sets of pairs of adjacent edges which do not necessarily have the maximum possible size. Indeed, if we find any  $k$  pairs of adjacent edges  $(e_i, f_i)_{i=1}^k$  in a graph  $G$  such that  $G - \bigcup_{i=1}^k \{e_i, f_i\}$  is connected, then by Lemma 4 we can assert that the maximum genus of  $G$  is at least  $k$ . This suggests that identifying a large number of pairs of adjacent edges whose removal leaves a connected subgraph can be utilised to obtain a simple approximation algorithm for the maximum genus. Indeed, in the following section we show that choosing the pairs of adjacent edges arbitrarily yields an effective approximation of maximum genus.

### 3 Algorithm

In this section we present a greedy algorithm for finding at least  $\gamma_M(G)/2$  pairs of adjacent edges while the rest of the graph remains connected. The idea is simple: if the removal of a pair of adjacent edges does not disconnect the graph, then we remove it.

To prove that the set output by Greedy-Max-Genus Algorithm always contains at least  $\gamma_M(G)/2$  pairs of adjacent edges we employ the following lemma, which can be easily proved either using Xuong's theorem or directly from Lemma 1.

**Lemma 5.** *Let  $G$  be a connected graph and let  $e$  be an arbitrary edge of  $G$  such that  $G - e$  is connected. Then*

$$\gamma_M(G) - 1 \leq \gamma_M(G - e) \leq \gamma_M(G).$$

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#### Greedy-Max-Genus Algorithm

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Input: Connected graph  $G$

Output: Set  $P$  of pairwise disjoint pairs of adjacent edges of  $G$  such that  $G - P$  is a connected spanning subgraph of  $G$

- 1:  $H \leftarrow G, P \leftarrow \emptyset$
  - 2: **repeat**
  - 3:     choose adjacent edges  $e, f$  from  $H$
  - 4:     **if**  $H - \{e, f\}$  is connected
  - 5:          $H \leftarrow H - \{e, f\}$
  - 6:          $P \leftarrow P \cup (e, f)$
  - 7: **until** all pairs of adjacent edges of  $H$  have been tested
  - 8: return  $P$
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The final ingredient for our Greedy-Max-Genus Algorithm is the following characterisation of graphs with maximum genus 0.

**Theorem 6.** *The following statements are equivalent for every connected graph  $G$ .*

- (i)  $\gamma_M(G) = 0$
- (ii) *No two cycles of  $G$  have a vertex in common.*
- (iii)  *$G$  contains no pair of adjacent edges whose removal leaves a connected graph.*

The equivalence (i)  $\Leftrightarrow$  (ii) in Theorem 6 was first proved by Nordhaus et al. in [18]. The equivalence (ii)  $\Leftrightarrow$  (iii) is easy to see, nevertheless it is its appropriate combination with Lemma 5 which yields the desired performance guarantee for Greedy-Max-Genus algorithm, as shown in the following theorem.

**Theorem 7.** *For every connected graph  $G$ , the set of pairs output by Greedy-Max-Genus Algorithm run on  $G$  contains at least  $\gamma_M(G)/2$  pairs of adjacent edges.*

*Proof.* Assume that the algorithm stops after the removal of  $k$  disjoint pairs of adjacent edges from  $G$ . For  $i \in \{0, 1, \dots, k\}$  let  $H_i$  denote the graph obtained from  $G$  by the removal of the the first  $i$  pairs of edges. By Lemma 5, the removal of a single edge from a graph can lower its maximum genus by at most one. Therefore, the removal of two edges can lower the maximum genus by at most two. It follows that  $\gamma_M(H_i) \geq \gamma_M(G) - 2i$  for each  $i$ ; in particular,  $\gamma_M(H_k) \geq \gamma_M(G) - 2k$ . From Theorem 6 we get that  $\gamma_M(H_k) = 0$ . By combining these expressions we get  $2k \geq \gamma_M(G)$ , which yields  $k \geq \gamma_M(G)/2$ , as desired.  $\square$

**Remark.** Let  $n$  and  $m$  denote the number of vertices and edges of  $G$ , respectively, and let  $k$  be the number of pairs of adjacent edges produced by Greedy-Max-Genus Algorithm run on  $G$ . An embedding of  $G$  with genus at least  $k$  can be constructed from the set of pairs of adjacent edges in time  $O(n + k \log n)$ , see the proof of Theorem 4.5 in [3] for details.

Observe that any maximal set of pairs of adjacent edges of  $G$  whose removal from  $G$  yields a connected graph can be output by Greedy-Max-Genus Algorithm run on  $G$ . Hence, as a corollary of Theorem 7 we obtain the following 2-approximate counterpart of Xuong's theorem.

**Theorem 8.** *Let  $G$  be a connected graph and let  $P$  be any inclusion-wise maximal set of disjoint pairs of adjacent edges of  $G$  whose removal leaves a connected subgraph. Then  $|P| \geq \gamma_M(G)/2$ .*

The following example shows that the bound of Theorem 8 is tight and Greedy-Max-Genus Algorithm can output the value  $\gamma_M(G)/2$  for infinitely many graphs  $G$ .

**Example 9.** Take the star  $K_{1,2n}$  where  $n$  is an arbitrary positive integer, replace every edge with a pair of parallel edges, and add a loop to every vertex of degree 2. Denote the resulting graph by  $G_n$ . Using Theorem 3 it is easy to see that  $\gamma_M(G_n) = 2n$ . Indeed, take a set  $P$  of  $2n$  disjoint pairs of adjacent edges, each consisting of a loop and one of its adjacent edges. Since the edges of  $G_n$  not in  $P$  form a spanning tree,  $P$  has maximum size with respect to the property that  $G - P$  is connected. Thus  $\gamma_M(G_n) = 2n$  by Theorem 3. On the other hand, consider a set  $P'$  of  $n$  disjoint pairs of adjacent edges that include only edges incident with the central vertex. The removal of these pairs from  $G_n$  leaves a spanning tree of  $G_n$  with a loop attached to every pendant vertex, so  $P'$  is a maximal set of pairs for which  $G_n - P'$  is connected. Since  $|P'| = n = \gamma_M(G_n)/2$ , our example confirms that the bound in Theorems 7 and 8 is best possible.

Example 9 also implies that processing vertices in the decreasing order with respect to their degrees does not necessarily lead to a better performance of the algorithm.

## 4 Implementation

To implement the algorithm it is clearly sufficient to consider all pairs of edges  $\{e, f\}$  with a common end-vertex and test whether removing the pair does not disconnect the graph. The running time is thus  $O((\tau + \rho) \sum_{i=1}^n d_i^2)$ , where  $\tau$  is the time required to test the connectivity,  $\rho$  is the time required to update the underlying data structure, and  $d_i$  is the degree of the  $i$ -th vertex. If the input graph is simple, then  $\sum_{i=1}^n d_i^2 = O(m^2/n)$  by [6]. If the input graph is not simple, we can preprocess it as follows. Let  $P = \emptyset$ . From every set  $F$  of pairwise parallel edges we repeatedly remove pairs of edges and add them into  $P$  until  $F$  contains at most two parallel edges. Similarly, from every set  $F$  of loops incident with a single vertex we remove pairs of loops and add them into  $P$  until  $F$  contains at most one loop. Let  $G'$  denote the resulting graph. Finally, the set  $P$  of pairs of adjacent edges is added to the set  $P'$  produced by Greedy-Max-Genus Algorithm on  $G'$ . It can be easily seen that in  $G'$  the sum of squares of the degrees is again in  $O(m^2/n)$  and that the preprocessing phase can be done in  $O(m)$ , where  $m$  and  $n$  is the number of edges and vertices of the input graph. Regarding the testing of connectivity, we have  $\tau = O(m)$  for instance by using DFS, in which case there is no need for additional updates of data structure and thus  $\rho = O(m)$ . Therefore, we obtain an implementation which reduces essentially to a series of connectivity tests and has running time  $O(m^3/n)$ . Using the dynamic graph algorithm for connectivity from [23] it is possible to support updates in  $\rho = O(\log^2 n / \log \log n)$  amortized time and queries in  $\tau = O(\log n / \log \log n)$  worst-case time. This yields the total running time  $O(m^2 \log^2 n / (n \log \log n))$ .

## 5 Discussion

We have presented an approximation algorithm for the maximum genus problem that for any connected graph  $G$  outputs an integer  $k$  such that  $\gamma_M(G)/2 \leq k \leq \gamma_M(G)$ . This result shows that the classical ideas dating back to Norhaus et al. [18] and Ringelsen [20], and to characterisations of maximum genus by Xuong [24] and Khomenko et al. [15], can be used also for efficient approximation of maximum genus. Our algorithm is much simpler than both the 4-approximation algorithm of Chen [3] and the precise polynomial-time algorithms for the maximum genus problem of Furst et al. [8] and Glukhov [9], outperforms the existing 4-approximation algorithm [3], and provides the first approximation of maximum genus that can be easily implemented. On the structural side, we have obtained a natural 2-approximation counterpart of Xuong's theorem.

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